

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/308,435A

DATE: 04/26/2001
TIME: 11:52:03

Input Set : A:\Astra561.app
Output Set: N:\CRF3\04262001\I308435A.raw

Does Not Comply
Corrected Diskette Needed

P.6

3 <110> APPLICANT: Astra Aktiebolag
5 <120> TITLE OF INVENTION: Vaccine Delivery System and Method of Production
7 <130> FILE REFERENCE: 1103326-0560
9 <140> CURRENT APPLICATION NUMBER: 09/308,435A
10 <141> CURRENT FILING DATE: 1999-05-19
12 <150> PRIOR APPLICATION NUMBER: PCT/SE99/00582
13 <151> PRIOR FILING DATE: 1999-04-09
15 <150> PRIOR APPLICATION NUMBER: SE 9801288-3
16 <151> PRIOR FILING DATE: 1998-04-14
18 <160> NUMBER OF SEQ ID NOS: 25
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1670
24 <212> TYPE: DNA
25 <213> ORGANISM: Helicobacter pylori
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (793)..(1572)
31 <400> SEQUENCE: 1
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36 gatttgattt tagggatta catgcaagtg aatgaaaaaaaa acattcaagc gtttgcggcc 180
38 aaacaataag gtaaaaaatg ccactcactc atttgaatga agaaaaatcaa cctaaaatgg 240
40 tggatatagg ggataaaagaa accactgaaa gaatgcgtc agcaagcgtt cgtatcagca 300
42 tgaataaaaga ggcttatgac gctattatca atcatggcgt caaaaaggggt ccggatttac 360
44 aaactgctat tattgctggg attatggggg ctaaaaagac aagcgaactc attcccatgt 420
46 gccatccaat catgctcaat ggggtggata ttgatatttt agaagaaaaa gagacttgta 480
48 gttttaaact ctatgcgaga gtcaaaactc aagctaaaac gggcgttagaa atggaaagcgc 540
50 taatgagtgt gagcgttaggg cttttaacca tttatgacat ggtgaaagcc attgataaga 600
52 gcatgacaat tagcgggtgt atgctgaaat ataaaagtgg aggcaaaagt ggggattata 660
54 acgctaaaaa atagaaaaag actgataatc taaagatatt agggtaaaat aacattttga 720
56 caacaaaagc gtgttggttg cttcggattt gttgttatag aagtctaaaaa tattacaatc 780
58 aaggatagaa cg atg aga gca aat aat cat ttt aaa gat ttt gca tgg aaa 831
59 Met Arg Ala Asn Asn His Phe Lys Asp Phe Ala Trp Lys
60 1 5 10
62 aaa tgc ctt tta ggc gcg agc gtg gtg gct tta tta gtg gga tgc agc 879
63 Lys Cys Leu Leu Gly Ala Ser Val Val Ala Leu Leu Val Gly Cys Ser
64 15 20 25
66 ccg cat att att gaa acc aat gaa gtc gct ttg aaa ttg aat tac cat 927
67 Pro His Ile Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His
68 30 35 40 45
70 cca gct agc gag aaa gtt caa gcg tta gat gaa aag att ttg ctt tta 975
71 Pro Ala Ser Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu
72 50 55 60
74 agg cca gct ttc caa tat agc gat aat atc gct aaa gag tat gaa aac 1023
75 Arg Pro Ala Phe Gln Tyr Ser Asp Asn Ile Ala Lys Glu Tyr Glu Asn
76 65 70 75

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78	aaa ttc aag aat caa acc gcg ctc aag gtt gaa cag att ttg caa aat	1071
79	Lys Phe Lys Asn Gln Thr Ala Leu Lys Val Glu Gln Ile Leu Gln Asn	
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82	caa ggc tat aag gtt att agc gta gat agc agc gat aaa gac gat ttt	1119
83	Gln Gly Tyr Lys Val Ile Ser Val Asp Ser Ser Asp Lys Asp Asp Phe	
84	95 100 105	
86	tct ttt gca caa aaa aaa gaa ggg tat ttg gcg gtt gct atg aat ggc	1167
87	Ser Phe Ala Gln Lys Lys Glu Gly Tyr Leu Ala Val Ala Met Asn Gly	
88	110 115 120 125	
90	gaa att gtt tta cgc ccc gat cct aaa agg acc ata cag aaa aaa tca	1215
91	Glu Ile Val Leu Arg Pro Asp Pro Lys Arg Thr Ile Gln Lys Lys Ser	
92	130 135 140	
94	gaa ccc ggg tta tta ttc tcc acc ggt ttg gac aaa atg gaa ggg gtt	1263
95	Glu Pro Gly Leu Leu Phe Ser Thr Gly Leu Asp Lys Met Glu Gly Val	
96	145 150 155	
98	tta atc ccg gct ggg ttt att aag gtt acc ata cta gag cct atg agt	1311
99	Leu Ile Pro Ala Gly Phe Ile Lys Val Thr Ile Leu Glu Pro Met Ser	
100	160 165 170	
102	ggg gaa tct ttg gat tct ttt acg atg gat ttg agc gag ttg gac att	1359
103	Gly Glu Ser Leu Asp Ser Phe Thr Met Asp Leu Ser Glu Leu Asp Ile	
104	175 180 185	
106	caa gaa aaa ttc tta aaa acc acc cat tca agc cat agc ggg ggg tta	1407
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108	190 195 200 205	
110	gtt agc act atg gtt aag gga acg gat aat tct aat gac gcg atc aag	1455
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114	agc gct ttg aat aag att ttt gca aat atc atg caa gaa ata gac aaa	1503
115	Ser Ala Leu Asn Lys Ile Phe Ala Asn Ile Met Gln Glu Ile Asp Lys	
116	225 230 235	
118	aaa ctc act caa aag aat tta gaa tct tat caa aaa gac gcc aaa gaa	1551
119	Lys Leu Thr Gln Lys Asn Leu Glu Ser Tyr Gln Lys Asp Ala Lys Glu	
120	240 245 250	
122	tta aaa ggc aaa aga aac cga taaaaacaaa taacgcataa gaaaagaacg	1602
123	Leu Lys Gly Lys Arg Asn Arg	
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141	20 25 30	
143	Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His Pro Ala Ser	
144	35 40 45	

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146 Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu Leu Arg Pro Ala
 147 50 55 60
 149 Phe Gln Tyr Ser Asp Asn Ile Ala Lys Glu Tyr Glu Asn Lys Phe Lys
 150 65 70 75 80
 152 Asn Gln Thr Ala Leu Lys Val Glu Gln Ile Leu Gln Asn Gln Gly Tyr
 153 85 90 95
 155 Lys Val Ile Ser Val Asp Ser Ser Asp Lys Asp Asp Phe Ser Phe Ala,
 156 100 105 110
 158 Gln Lys Lys Glu Gly Tyr Leu Ala Val Ala Met Asn Gly Glu Ile Val
 159 115 120 125
 161 Leu Arg Pro Asp Pro Lys Arg Thr Ile Gln Lys Lys Ser Glu Pro Gly
 162 130 135 140
 164 Leu Leu Phe Ser Thr Gly Leu Asp Lys Met Glu Gly Val Leu Ile Pro
 165 145 150 155 160
 167 Ala Gly Phe Ile Lys Val Thr Ile Leu Glu Pro Met Ser Gly Glu Ser
 168 165 170 175
 170 Leu Asp Ser Phe Thr Met Asp Leu Ser Glu Leu Asp Ile Gln Glu Lys
 171 180 185 190
 173 Phe Leu Lys Thr Thr His Ser Ser His Ser Gly Gly Leu Val Ser Thr
 174 195 200 205
 176 Met Val Lys Gly Thr Asp Asn Ser Asn Asp Ala Ile Lys Ser Ala Leu
 177 210 215 220
 179 Asn Lys Ile Phe Ala Asn Ile Met Gln Glu Ile Asp Lys Lys Leu Thr
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 191 <211> LENGTH: 1670
 192 <212> TYPE: DNA
 193 <213> ORGANISM: Helicobacter pylori
 195 <220> FEATURE:
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 208 tggatatagg ggataaagaa accactgaaa gaatcgctc agcaagcggt cgtatcagca 300
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 218 taatgagtgt gagcgttaggg cttttaacca tttatgacat ggtgaaagcc attgataaga 600
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 224 caacaaaagc gtgttggttg cttcggattt gttgttatag aagtctaaaa tattacaatc 780

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228		1			5						10							
230	aaa	tgc	ctt	tta	ggc	gcg	agc	gtg	gtg	gct	tta	gtg	gga	tgc	agc	879		
231	Lys	Cys	Leu	Leu	Gly	Ala	Ser	Val	Val	Ala	Leu	Leu	Val	Gly	Cys	Ser		
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234	ccg	cat	att	att	gaa	acc	aat	gaa	gtc	gct	ttg	aaa	ttg	aat	tac	cat	927	
235	Pro	His	Ile	Ile	Glu	Thr	Asn	Glu	Val	Ala	Leu	Lys	Leu	Asn	Tyr	His		
236	30				35						40				45			
238	cca	gct	agc	gag	aaa	gtt	caa	gcg	tta	gat	gaa	aag	att	ttg	ctt	tta	975	
239	Pro	Ala	Ser	Glu	Lys	Val	Gln	Ala	Leu	Asp	Glu	Lys	Ile	Leu	Leu			
240	50				55						60							
242	agg	cca	gct	ttc	caa	tat	agc	gat	aat	atc	gct	aaa	gag	tat	gaa	aac	1023	
243	Arg	Pro	Ala	Phe	Gln	Tyr	Ser	Asp	Asn	Ile	Ala	Lys	Glu	Tyr	Glu	Asn		
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256	110				115						120				125			
258	gaa	att	gtt	tta	cgc	ccc	gat	cct	aaa	agg	acc	ata	cag	aaa	aaa	tca	1215	
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264	145				150						155							
266	tta	atc	ccg	gct	ggg	ttt	att	aag	gtt	acc	ata	cta	gag	cct	atg	agt	1311	
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270	ggg	gaa	tct	ttg	gat	tct	ttt	acg	atg	gat	ttg	agc	gag	ttg	gac	att	1359	
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288	240				245						250							
290	tta	aaa	ggc	aaa	aga	aac	cga	taaaaaacaaa	taacgcataa	gaaaagaacg						1602		

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291 Leu Lys Gly Lys Arg Asn Arg
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 308 Leu Gly Ala Ser Val Val Ala Leu Leu Val Gly Cys Ser Pro His Ile
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 311 Ile Glu Thr Asn Glu Val Ala Leu Lys Leu Asn Tyr His Pro Ala Ser
 312 35 40 45
 314 Glu Lys Val Gln Ala Leu Asp Glu Lys Ile Leu Leu Arg Pro Ala
 315 50 55 60
 317 Phe Gln Tyr Ser Asp Asn Ile Ala Lys Glu Tyr Glu Asn Lys Phe Lys
 318 65 70 75 80
 320 Asn Gln Thr Ala Leu Lys Val Glu Gln Ile Leu Gln Asn Gln Gly Tyr
 321 85 90 95
 323 Lys Val Ile Ser Val Asp Ser Ser Asp Lys Asp Asp Phe Ser Phe Ala
 324 100 105 110
 326 Gln Lys Lys Glu Gly Tyr Leu Ala Val Ala Met Asn Gly Glu Ile Val
 327 115 120 125
 329 Leu Arg Pro Asp Pro Lys Arg Thr Ile Gln Lys Lys Ser Glu Pro Gly
 330 130 135 140
 332 Leu Leu Phe Ser Thr Gly Leu Asp Lys Met Glu Gly Val Leu Ile Pro
 333 145 150 155 160
 335 Ala Gly Phe Ile Lys Val Thr Ile Leu Glu Pro Met Ser Gly Glu Ser
 336 165 170 175
 338 Leu Asp Ser Phe Thr Met Asp Leu Ser Glu Leu Asp Ile Gln Glu Lys
 339 180 185 190
 341 Phe Leu Lys Thr Thr His Ser Ser His Ser Gly Gly Leu Val Ser Thr
 342 195 200 205
 344 Met Val Lys Gly Thr Asp Asn Ser Asn Asp Ala Ile Lys Arg Ala Leu
 345 210 215 220
 347 Asn Lys Ile Phe Ala Asn Ile Met Gln Glu Ile Asp Lys Lys Leu Thr
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09/28, 435A 6

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<213> Helicobacter pylori

> C2117 ← MANDATORY numeric identifier and
response needed

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where are amino acids?

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/308,435A

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Input Set : A:\Astra561.app

Output Set: N:\CRF3\04262001\I308435A.raw

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